Mungbean (*Vigna radiata* (L.) R. Wilczek): Progress in Breeding and Future Challenges

Abstract

Mungbean (*Vigna radiata* (L.) R. Wilczek) is a short duration, farmer preferred pulse crop of warm-season. The crop has shown a balanced growth worldwide, especially in developing countries. Mungbean being a great source of protein with higher folate and iron levels attracts high demand and price in the market making the farmers happy and satisfied. Moreover, it can fix atmospheric nitrogen through symbiosis with nitrogen-fixing bacteria, making it perfect for rice based cropping systems and intercropping with other crops. Despite having so many benefits, mungbean has been a neglected crop compared to other pulses with few efforts aiming at its breeding and development. Higher productivity, breeding for biotic and abiotic stresses resistance, nutritional quality improvement is future challenges for mungbean breeders. Several researchers are working in the direction of collecting and maintaining mungbean genetic resources. Mutation breeding and genetic engineering has also enhanced in mungbean varietal improvement. Genomic information is lacking compared to other legume species. However, the recent successful sequencing of mungbean genome has opened new vistas into the crop's R&D. It is a self-pollinated pulse with small genome size, which could be used as a model for studying other legumes. The mungbean breeders at present times aim to identify useful alleles from diverse germplasm and markers closely associated with desirable traits. The high-throughput marker genotyping system has now made it feasible to pinpoint the exact gene locations and mutations contributing target phenotypes. The present review is an overview of the present conventional and molecular breeding status in the crop and summary of efforts in the utilization of genetic information and genomic resources for further mungbean improvement.

Introduction and importance

Mungbean (*Vigna radiata* (L.) R. Wilczek), commonly known as green gram, is an essential legume crop grown and consumed globally. It is a rice source of protein, carbohydrates, starch, vitamin C, isoflavonoid (vitexin), folate, iron and zinc (Cao et al. 2011; Keatinge et al. 2011). The demands for this pulse have increased looking into these benefits. It is believed that farmers prefer this pulse even in the present times of climate change due to its three benefits *viz*., nutrition, benefit to soil and short duration (Graham and Vance 2003; Keatinge et al. 2011). In addition to this, mungbean has low input requirement, suitable for cereal-based crop rotation, intercropping with sugarcane and maize, good performance under heat and drought stress. Although, the risks due to changing climate cannot be neglected though as situations like drought, salinity, heat stress, etc. has made the crop production, a variable. Various varieties of mungbean are used differently worldwide based on consumer requirement of particular region. They are used as dry grains (dahl), vegetable bean sprouts, flour, soups, porridge, transparent noodles made of starch, mungbean paste used as an ingredient of sweets and cakes. In, China and Indian (Ayurvedic) medicine mungbean has therapeutic purposes owing to its high levels phenols, flavonoids, vitexin and isovitexin (Kim et al. 2012). Crop residues are also utilized as animal feed and green manure (Pataczek et al. 2018; Nair et al. 2019).Mungbean is suitable for semi-arid to sub humid lowland tropics and subtropics with average annual rainfall of 600–1000 mm. Being grown during the warm season in absence of frost condition, it has a crop duration of 90–120 days from planting to maturity. The optimum temperature for planting is 15 °C and 20–30 °C during crop growth

(Oplinger et al. 1990). The flowering in the crop gets affected by day length. Short days accelerate flowering, while long days delay them (Agarwal and Poehlman 1977). Water stress during the reproductive stage has negative impact on flowing leading to decreased total yield (Raza et al. 2012). Excessive rainfall increases humidity making congenial conditions for diseases and pest infestation (Oplinger et al. 1990).

Production status

Although, India is the largest producer and consumer of mungbean accounting for >50% of global annual production, the average yield is merely 420 kg/ha which is very less compared to global average of 721 kg/ha (Nair et al. 2012). Over past few years, area of mungbean in India has increased, currently being approx. 3.8mha giving produce of about 1.6 mt. Among the Indian states, Rajasthan (31%) leads in area and production, followed by Maharashtra (11%). Myanmar being world’s largest exporter of mungbean accounts for 70% of mungbean imported in India. There is 1.2 m ha area of the crop in Myanmar currently giving almost equal produce compared to India (1.59mt). Other major countries contributing to mungbean production includes China, Kenya, Tanzania, Thailand, Indonesia, Bangladesh, Pakistan, etc.

Taxonomy, Genetic Resources and Domestication

Mungbean is a self-pollinated diploid crop with chromosome number of 2n=2x=22 (Arumuganathan and Earle 1991). This warm-season, frost intolerant, fast-growing pulse crop belongs to the genus *Vigna,* subgenus *Ceratotropis* in the papilionoid subfamily of the Fabaceae. It is mainly grown by farmers of South, East, and Southeast Asia with small land holdings. The key aim of breeders is to accumulate beneficial alleles from various parental lines into a new plant variety. Therefore, the availability of mungbean genetic resources having rich genetic variation is fundamental for success of crop improvement programs. The first step in finding superior alleles or the individuals carrying them is to secure a germplasm pool with high genetic diversity. A number of research institutes have been established for mungbean germplasm conservation activities and cultivar development. Germplasm of mungbean is being maintained at AVRDC-The World Vegetable Center, Taiwan; National Bureau of Plant Genetic Resources (NBPGR) of the Indian Council of Agricultural Research (ICAR); the Institute of Crop Germplasm Resources of the Chinese Academy of Agricultural Sciences; the Plant Genetic Resources Conservation Unit of the University of Georgia, USA and the University of the Philippines (Kim et al. 2015). AVRDC- World Vegetable Center, Taiwan, holds the largest *Vigna*germplasm collection of the world made up of 11,832 accessions of mungbean (10,673 *Vigna*species, 881 *V. angularis*, 278 *V. unguiculata*), as vital resources for cultivar improvement through interspecific hybridization. The institute maintains a core collection of 1481 accessions with a mini-core collection of 296 accessions based on phenotypic and molecular characterization (Shanmuga sundaram et al. 2009). On the basis of archaeological evidence, diversity data and morphological studies, it is believed that mungbean was domesticated in India ~3500 years ago (Fuller and Harvey 2006; Jain and Mehra 1980; Singh et al. 1975). The wild form of mungbean, *Vignaradiata* var. *sublobata*, is however, indigenous to the subtropical and tropical regions of Australia and widely distributed throughout Africa and Asia (Lawn and Cottrell 1988). Studies based on protein variation and enzyme diversity conclude that modern mungbean cultivars are a result of multiple rounds of domestication (Lambrides and Godwin 2007).

Current state of mungbean breeding

Indeterminate growth habit, late and non-synchronous maturity, abiotic and biotic stresses are factors that cause depletion in mungbean harvest index (Fernandez and Shanmugasundaram1988; Alam Mondal et al. 2011). Slightly delayed harvesting also causes major yield loss as mature and dried pods shatter and get exposed to pest and pathogen attack. Multiple harvests is performed to prevent such loss which results in additional costs beared by producers. Thus, synchronous maturity is a key objective of mungbean breeding programs that can result in cost-effective harvesting. Although, the genetic basis of this trait is still unknown (Afzal et al. 2003; Chen et al. 2008).

Traditional Breeding

Conventional mungbean breeding aims at high yields, uniform maturity, and resistance to diseases like powdery mildew, *Cercospora* leaf spot, mungbean yellow mosaic virus(MYMV) and pest like mungbean pod borer, bruchids and bean flies (Tomooka et al.2005). In any crop species, wild resources are mined and utilized for useful genes as the cultivated germplasm has lost a number of useful alleles during domestication andmodern breeding programs (Kumar et al. 2011; Hyten et al. 2006; Tanksley and McCouch 1997). Abruchid-resistant mungbean cultivar was successfully developed utilizing TC1996, a wild mungbean relativeresistant to bruchid beetles (*Callosobruchus chinensis* and *C. maculatus*) (Somta et al. 2008; Talekar 1988). Also, MYMV resistant cultivars have been developed from *Vigna mungo*, another wild relative species of mungbean (Basak et al. 2005; Gill et al. 1983). Such success stories have made researchers to further realize the importance of conserving and maintaining germplasm in order to sustain mungbean genetic resources.

Molecular Marker-Assisted Breeding

Molecular markers are tags that help breeders to identify loci or genomic regions associated with desirable traits. Finding the phenotypic trait governed by a segment of DNA through the use of molecular markers is more accurate compared to traditional breeding (Collard and Mackill 2008). Be it genetic diversity studies, construction of linkage maps or identifying QTLs for desirable traits, molecular makers are always preferred as they are cost effective, precise and reduce time and input resources. The recent availability of whole-genome sequencing and high-throughput genotyping systems have aided molecular genetics studies (Huang et al. 2010; Zhou et al. 2015). Markers have been used for many resistance studies in mungbean and have been successfully deployed in mungbean improvement. Protein markers were used for studies like phylogenetic relationship between *Vigna* species, detection of polymorphic between MYMV-resistant and susceptible genotypes (Kole and Panigrahi 2001; Pattnaik and Kole 2002). Since these markers were limited in quantity, researchers gave DNA-based markers upper hand. Restriction fragment length polymorphism (RFLP) markers were the first to be used in mungbean for traits like the genetics of bruchid resistance, seed weight, seed size and powdery mildew (Young et al. 1992; Fatokun et al. 1992; Menancio-Hautea et al. 1992). Molecular marker studies in mungbean became common with the introduction of random amplified polymorphic DNA (RAPD) markers. They were used to assess genetic diversity in germplasm, cultivars and map biotic resistance traits like MYMV and bruchid beetles (Santalla et al. 1998; Lakhanpaul et al. 2000; Selvi et al. 2006; Chenet al. 2007). Utilizing an F_2 mapping population (cross between *V. radiata* ssp. *radiata* and *V. radiata* ssp. *sublobata),* Lambrides et al. (2000) integrated RFLP and RAPD markers to construct a genetic map having 12 linkage groups. Chattopadhyay et al. (2005) used a combination of RAPD and inter simple sequence repeat (ISSR) markers to assess genetic diversity in the crop. The AFLP markers further improved diversity and trait mapping studies (Singh et al. 2013; Chaitieng et al. 2002; Srinives et al. 2010).

Simple sequence repeat (SSR) markers are highly reproducible and informative markers of breeders' choice as they are co-dominant, highly polymorphic and easy to generate. The first SSR markers reported in mungbean were generated from 6 SSR sequences with 5 different types of motifs (Yu et al. 1999). Adzuki bean shares close phylogenetic relationship with mungbean. Thus, the SSR markers from adzuki bean were successfully detected during genetic diversity assessment various cultivated and wild mungbean accessions with higher allelic polymorphisms in the latter (Sangiri et al. 2008).The SSR markers were then generated from *Vigna* species genomic and transcriptomic sequences (Somta et al. 2009; Tangphatsornruanget al. 2009; Gupta et al. 2014; Chen et al. 2015a). A genetic map with 150 SSR markers across 11 linkage groups was constructed in mungbean (Kajonphol et al. 2017).SSR markers were also used in mungbean with partial linkage maps to identify traits like resistance to powdery mildew, *Cercospora* leaf spot, phytic acid content, etc., (Chankaewet al. 2011; Kasettranan et al. 2010; Sompong et al. 2012) and assess germplasm genetic diversity (Schafleitner et al. 2015). Prior to the emergence of high-throughput genotyping and next generation sequencing (NGS), limited polymorphic genetic markers were available to quantify population genetic diversity. Limit in the number of markers can create biased QTL identification due to inappropriate allelic diversity representation in genome (Moragues et al. 2010). SNPs are now most preferably used genetic markers as they are single base, biallelic, co-dominant and uniformly distributed across the genome (Brumfield et al. 2003). Transcriptome sequencing and Illumina Hi-Seq sequencing were utilized for study of two mungbean cultivars (Seonhwanogdu and Jangannogdu) genomes to study resistance to stink bug (*Riptortus clavatus*) and adzuki bean weevil (*Callosobruchus chinensis*) (Moe et al. 2011; Van et al. 2013). Single-nucleotide polymorphic (SNP) markers were detected in mungbean followed by the completion of whole genome sequence of cultivar VC1973A (Kang et al. 2014). Following the draft genome assembly, transcriptome assemblies were analysed from 22 accessions of 18 *Vigna* species providing better insights into the evolution of *Vigna* species. Utilizing a high-density genetic map, total of 2748 scaffolds were anchored on 11 pseudochromosomes spanning 431 Mbp. This genotyping-by-sequencing (GBS) based genetic map comprised of 1321 SNP markers developed from an F_6 recombinant inbred lines (RILs) population. Population had 190 RILs derived from a cross between Seonhwanogdu (*VC1973A*) and Gyeonggijaerae5 (V2985). Estimated genome size covered in this map is about 80% (579 Mbp). Also, 22,427 high-confidence protein-coding genes were annotated which is great compared to previous low-resolution linkage maps and fragmental genomic sequence information. Across the mungbean genome, a total of 2,922,833 SNPs were revealed in wild and cultivated varieties with 6.78 per 1 kbp frequency. 63,294 SNPs were located in protein-coding sequence (CDS) regions, while 30,405 showed non-synonymous changes. Moreover, from 342,853 insertions/deletions (InDels), 55,689 were located around genic regions, causing frame-shifts in a1057 genes.

There developments have increased the likelihood of vast number of markers' production which can lead to more projects of GBS and re-sequencing exploring new dimensions in the crop (Kang et al. 2014; Schafleitner et al. 2016). It has improvised the state of mungbean breeding.

Functional and Translational Genomics

The transcriptome data and molecular markers developed from it are highly informative as they are based on variations present in expressed genome regions. After the use expressed sequence tag (EST) sequences in crops, data mining has become a fast, cost-effective way of developing markers contributing to functional genomics studies in mungbean. Moe et al. (2011) used 12,596 EST sequences from cv. Jangannogdu that identified 2299 SSR motifs in 1848 EST sequences. 97 PCR primer sets were successfully designed and amplified in two mungbean cultivars, TM96-2 and TARM-18 from the same which contained approx. 45% and 55% SSR motifs located in CDS and untranslated regions (UTRs), respectively. The NCBI mungbean database was used to identify EST-SSR markers via data mining without bearing extra sequencing costs (Chavan and Gacche 2014). An SSR-enriched library was constructed from six mungbean genotypes *viz.* ACC41, VC1973A, V2709, C01478, C01558, and C01579 that identified 308,509 SSR motifs (Wang et al. 2015). To characterize and validate SSR markers detected from in-silico EST-SSR markers, the mungbean transcriptome was sequenced using Illumina paired-end sequencing (Chen et al. 2015). These studies resulted in the development various markers leading to advances in linkage map and QTL mapping analysis, thus facilitating mungbean breeding.

Translational genomics can be defined as the complete study of genomic information from a species utilized to analyse other species (Varshney et al. 2015). Genomic information can be applied from model species to crops that have rarely been studied previously, thus helping breeders improve various other crops with ease (Stacey and Vanden Bosch 2005). Currently post the genomic sequences for mungbean has been available, studies are being performed to characterize the mungbean genome using translational genomics. Genome-wide comparisons between mungbean and *Arabidopsis* identified flowering genes in mungbean (Kim et al. 2014). Out of 207 flowering genes in *Arabidopsis,* 129 genes were found homologous to mungbean genes. Also, comparison between mungbean and soybean genomes identified five putative flowering-related genes of mungbean in homology with soybean flowering genes (Kim et al. 2014). Comparative and synteny analysis between mungbean and soybean found several mungbean QTLs and putative genic loci associated with important traits *viz.* plant height, flowering, seed weight, seed oil content, seed size/germination, etc. (Kang et al. 2014; Kim et al. 2015; Hwang et al. 2017). Translational genomics studies in mungbean will expedite molecular studies leading to functional characterization of desirable genes

Genetic Transformation and Regeneration in Mungbean

Traditional breeding have achieved limited success in developing new varieties of mungbean owing to narrow genetic variation in the crop. Similar set of parental lines have been used repeatedly for varietal development. In addition to the effective utilization of germplasm, biotechnological tools are also a powerful tool to overcome drawbacks in development of elite mungbean breeding lines. Tissue culture allows regeneration of plants from transformed plant cells (Chandra and Pental 2003). First genetic transformation report in mungbean was conducted by Jaiwal et al. (2001) using hypocotyls and primary leaves. A generalized plant regeneration protocol using primary leaf explants was developed in mungbean showing ~90% survival rate (Mahalakshmi et al. 2006). Cotyledonary node explants were used for the successfully expression of the insecticidal α-amylase inhibitor-1gene from and the bialaphos resistance (*bar*) gene in mungbean (Sonia et al. 2007). Improvement for other important mungbean traits from various crops like *Phaseolus vulgaris*, mustard have been worked out in different studies for traits like disease resistance, drought and salt stress tolerance (Vijayan and Kirti 2012; Yadav et al. 2012; Baloda et al. 2017). Regeneration protocols have been reported in mungbean through embryogenesis and organogenesis (Kaviraj et al. 2006; Sivakumar et al. 2010; Himabindu et al. 2014; Rao et al. 2005). Very few regeneration studies which used cotyledonary node explants were successful (Vijayan et al. 2006; Amutha et al. 2006; Yadav et al. 2010; Sagare and Mohanty 2015). Limited studies could report production of stable transformed mungbean transgenic having stably inherited transgenes (Mahalakshmi et al. 2006; Sonia et al. 2007; Vijayan and Kirti 2012; Yadav et al. 2012; Baloda et al. 2017). The recalcitrant nature in mungbean tissue culture is the reason for lagging of transgenics report in the crop (Eapen 2008; Varshney et al. 2015). Application of recent biotechnological tools like genetic engineering, clustered regularly interspaced short palindromic repeats (CRISPR) to food crops can be positive tools in mungbean cultivar development overcoming the limitations of traditional breeding (Ran et al. 2013).

Mutation Breeding

In case of traditional breeding methods, the key bottleneck to enhancing yields in mungbean is the low genetic variability in germplasm and continuous decline in the genetic diversity. Thus, artificial mutations provide the way forward for crop improvement. Physical and chemical mutagens are considered effective ways to induce mutations subsequently creating genetic variability. Several mutagens like ethyl methane sulfonate (EMS), sodium azide (SA), hydrazine hydrate (HZ) and gamma rays have been used in mungbean. Various mungbean genotypes treated with EMS and gamma rays lead to new cultivars with higher yields and increased resistance to bean fly infestation (Khan and Goyal 2009; Wani 2006). The use of EMS and HZ as mutagens in mungbean showed significant increase in the number of branches, pods and seed yield in mutants (Wani 2006). Mutants obtained from SA, EMS, and gamma rays displayed a wide range of morphological and physiological features like variegated leaves, synchronous pod maturity, etc (Sangsiri et al. 2007; Tah and Saxena 2009; Auti and Apparao 2009).

Mungbean suffers serious yields losses from pathogens like viruses, fungi, bacteria and nematodes affecting tissues including seeds, leaves, flowers, roots and stems. Seed germination, shoot development, flower development are other detrimental pathogen impact ultimately reduced yields. MYMV is one of the most studied mungbean viruses with its full reference genome available (Morinaga et al. 1993). The MYMV-infected plants show yellow discoloration leading to approx. 85% yield losses (Karthikeyan et al. 2014). Development of fully-resistant cultivars haven’t been successful yet in mungbean, although targeted mutagenesis and sequencing techniques can be a path forward for breeders to identify the casual variations induced by mutagens via forward genetics analysis (Kang et al. 2014). The cultivars released through mutation breeding increases genetic diversity by being used as breeding materials for conventional plant breeding leading to the genetic improvement of mungbean. Mutation-assisted plant breeding is capable of play creating customized crop cultivars to sustain in the era of global climate change and food insufficiency.

Conclusion and Prospects

Due to its farmer preference and high nutritional contents, mungbean has gain edits importance among other pulses. Earlier mungbean received less attention being a crop of interest only for developing countries and the lack of genomic information. The reference genome sequence of mungbean published in 2014 encouraged breeders and researchers to study the genetic and genomic backgrounds of ergonomically important traits in the crop. In recent times, there has been subsequent increase in genomic resources of mungbean, thus generating huge amount of valuable data. Various markers and QTLs have been developed and identified based on the currently available genomic information and phenotypic data. Researchers are screening valuable resources to find QTLs and locating casual genes for traits of their interest. Furthermore, the germplasm collections can be utilized for investigating allelic variations; genome-wide association studies (GWAS) to locate candidate genes. Mungbean has all the properties to be a model plant system for carrying out genomic studies in legumes.

NOTE:

The study highlights the efficacy of " Ayurvedic" which is an ancient tradition, used in some parts of India. This ancient concept should be carefully evaluated in the light of modern medical science and can be utilized partially if found suitable.

References

Afzal M, Bakr M, Luna NK et al (2003) Registration of ‘Barimung-5’ mungbean. Crop Sci43:2304–2306

Aggarwal DV, Poehlman JM (1977) Effects of photoperiod and temperature on flowering in mungbean*Vignaradiata*(L.) Wilczek. Euphytica 26:207–219

AlamMondal MM, Ali Fakir MS, Juraimi AS et al (2011) Effects of flowering behavior and podmaturity synchrony on yield of mungbean [‘*Vignaradiata*’(L.) Wilczek]. Aust J Crop Sci5(8):945–953

Arumuganathan K, Earle E (1991) Nuclear DNA content of some important plant species. PlantMolBiol Report 9:208–218

Auti S, Apparao B (2009) Induced mutagenesis in mungbean (*Vignaradiata*(L.) Wilczek). In: ShuQY (ed) Induced plant mutations in the genomics era. FAO/IAEA, Rome, pp 107–110

Baloda A, Madanpotra S, Aiwal PKJ (2017) Transformation of mungbean plants for salt anddrought tolerance by introducing a gene for an osmoprotectant glycine betaine. J Plant StressPhysiol 3:5–11

Basak J, Kundagrami S, Ghose T, Pal A (2005) Development of yellow mosaic virus (YMV) resistancelinked DNA marker in *Vignamungo*from populations segregating for YMV-reaction.Mol Breed 14:375–383

Brumfield RT, Beerli P, Nickerson DA, Edwards SV (2003) The utility of single nucleotide polymorphismsin inferences of population history. Trends EcolEvol 18:249–256

Cao D, Li H, Yi J, Zhang J, Che H, Cao J et al (2011)Antioxidant properties of the mungbean flavonoids onalleviating heat stress. PLOS One 6:e21071

Chaitieng B, Kaga A, Han OK, Wang XW, Wongkaew S,Laosuwan P, Tomooka N, Vaughan DA (2002)Mapping a new source of resistance to powderymildew in mungbean. Plant Breed 121:521–525

Chandra A, Pental D (2003) Regeneration and genetic transformation of grain legumes: an overview.CurrSci 84:381–387

Chankaew S, Somta P, Sorajjapinun W, Srinives P (2011) Quantitative trait loci mapping of*Cercospora*leaf spot resistance in mungbean, *Vignaradiata*(L.) Wilczek. Mol Breed28:255–264

Chattopadhyay K, Ali MN, Sarkar H et al (2005) Diversity analysis by RAPD and ISSR markersamong the selected mungbean [*Vignaradiata*(L.) Wilczek] genotypes. Indian J Genet PlantBreed 65:173–175

Chavan SP, Gacche R (2014) Identification and characterization of EST-SSRs in mungbean.Webmedcentral 5:WMC004598. https://doi.org/10.9754/journal.wmc.2014.004598

Chen HM, Liu CA, Kuo CG, Chien CM, Sun HC,Huang CC, Lin YC, Ku HM (2007) Development of amolecular marker for a bruchid (*Callosobruchuschinensis* L.) resistance gene in mungbean. Euphytica157:113–122

Chen L-R, Markhart AH, Shanmugasundaram S, Lin T-Y (2008) Early developmental and stressresponsive ESTs from mungbean, *Vignaradiata*(L.) Wilczek, seedlings. Plant Cell Rep27:535–552

Chen H, Wang L, Wang S et al (2015) Transcriptome sequencing of mung bean (*Vignaradiata*L.)genes and the identification of EST-SSR markers. PLoS One 10:e0120273

Collard BC, Mackill DJ (2008) Marker-assisted selection: an approach for precision plant breedingin the twenty-first century. Philos Trans R SocLondSer B BiolSci 363:557–572

Eapen S (2008) Advances in development of transgenic pulse crops. BiotechnolAdv 26:162–168

Fatokun CA, Menancio-Hautea DI, Danesh D, Young ND (1992) Evidence for orthologous seedweight genes in cowpea and mung bean based on RFLP mapping. Genetics 132:841–846

Fernandez G, Shanmugasundaram S (1988) The AVRDC mungbean improvement program: thepast, present and future. In: Shanmugasundaram S, McLean BT (eds) Mungbean: proceedingsof the second international symposium. AVRDC, Shanhua, pp 58–70

Fuller DQ, Harvey EL (2006) Thearchaeobotany of Indian pulses: identification, processing andevidence for cultivation. Environ Archaeol 11:219–246

Gill A, Verma M, Dhaliwal H, Sandhu T (1983) Interspecific transfer of resistance to mungbeanyellow mosaic virus from *Vignamungo*to *Vignaradiata*. CurrSci 52:31–33

Graham PH, Vance CP (2003) Legumes: importance and constraints to greater use. Plant Physiol131:872–877

Gupta SK, Bansal R, Gopalakrishna T (2014) Developmentand characterization of genic SSR markers formungbean (*Vignaradiata* (L.) Wilczek). Euphytica195:245–258

Himabindu Y, Reddy M, Chandrasekhar T (2014) *In vitro* regeneration of green gram (*Vignaradiate* (L.) Wilczek) cultivar Vamban-2 using cotyledonary nodes. CIB Tech J Biotechnol 3:11–15

Huang X, Sang T, Zhao Q et al (2010) Genome-wide association studies of 14 agronomic traits inrice landraces. Nat Genet 42:961–967

Hwang WJ, Ha J, Lee T et al (2017) A candidate flowering gene in mungbean is homologous to asoybean *Phytochrome A* gene. Euphytica 213:79. https://doi.org/10.1007/s10681-017-1866-8

Hyten DL, Song Q, Zhu Y et al (2006) Impacts of genetic bottlenecks on soybean genome diversity.ProcNatlAcadSci 103:16666–16671

Jain H, Mehra K (1980) Evolution, adaptation, relationships, and uses of the species of *Vigna*cultivated in India. In: Summerfield RJ, Bunting AH (eds) Advances in legume science. RoyalBotanic Gardens, Kew, pp 459–468

Jaiwal PK, Kumari R, Ignacimuthu S et al (2001) *Agrobacterium tumefaciens*-mediated genetictransformation of mungbean (*Vignaradiata*L. Wilczek) – a recalcitrant grain legume. PlantSci 161:239–247

Kajonphol T, Sangsiri C, Somta P, Toojinda T, Srinives P(2017) SSR map construction and quantitative traitloci (QTL) identification of major agronomic traits inmungbean (*Vignaradiata* (L.) Wilczek). SABRAO JBreed Genet 44(1):71–86

Kang YJ, Kim SK, Kim MY et al (2014) Genome sequence of mungbean and insights into evolutionwithin *Vigna*species. Nat Commun 5:5443

Karthikeyan A, Shobhana VG, Sudha M et al (2014) Mungbean yellow mosaic virus (MYMV): athreat to green gram (*Vignaradiata*) production in Asia. Int J Pest Manag 60:314–324

Kasettranan W, Somta P, Srinives P (2010) Mapping of quantitative trait loci controlling powderymildew resistance in mungbean (*Vignaradiata*(L.) Wilczek). J Crop SciBiotechnol13:155–161

Kaviraj C, Kiran G, Venugopal R et al (2006) Somatic embryogenesis and plant generation fromcotyledonary explants of green gram [*Vignaradiata*(L.) Wilczek]- a recalcitrant grain legume.In Vitro Cell DevBiol-Plant 42:134–138

Keatinge J, Easdown W, Yang R et al (2011) Overcoming chronic malnutrition in a future warmingworld: the key importance of mungbean and vegetable soybean. Euphytica 180:129–141

Khan S, Goyal S (2009) Improvement of mungbean varieties through induced mutations. AfricanJ Plant Sci 3:174–180

Kim DK, Jeong SC, Gorinstein S, Chon SU (2012) Totalpolyphenols, antioxidant and antiproliferative activitiesof different extracts in mungbean seeds andsprouts. Plant Foods Hum Nutr 67:71

Kim SK, Lee T, Kang YJ et al (2014) Genome-wide comparative analysis of flowering genesbetween *Arabidopsis* and mungbean. Genes Genomics 36:799–808

Kim SK, Nair RM, Lee J, Lee S-H (2015) Genomic resources in mungbean for future breedingprograms. Front Plant Sci 6:626. https://doi.org/10.3389/fpls.2015.00626

Kole C, Panigrahi J (2001) *Vignaglabrescens* is a naturalallopolyploid of *V. radiata* and *V. umbellata*: evidencesfrom seed protein electrophoresis. Crop Res22:121–128

Kumar J, Choudhary AK, Solanki RK, Pratap A (2011) Towards marker-assisted selection inpulses: a review. Plant Breed 130:297–313

Lakhanpaul S, Chadha S, Bhat KV (2000) Randomamplified polymorphic DNA (RAPD) analysis inIndian mung bean (*Vignaradiata* (L.) Wilczek)cultivars. Genetica 109(3):227–34

Lambrides C, Godwin I (2007) Mungbean. In: Kole C (ed) Pulses, sugar and tuber crops. Springer,Berlin, pp 69–90

Lambrides C, Lawn R, Godwin I et al (2000) Two genetic linkage maps of mungbean using RFLPand RAPD markers. Aust J Agric Res 51:415–425

Lawn R, Cottrell A (1988) Wild mungbean and its relatives in Australia. Biologist 35(5):267–273

Mahalakshmi LS, Leela T, Kumar SM et al (2006) Enhanced genetic transformation efficiency ofmungbean by use of primary leaf explants. CurrSci 91:93–99

Menancio-Hautea D, Kumar L, Danesh D, Young N (1992) A genome map for mungbean [*Vignaradiata*(L.) Wilczek] based on DNA genetic markers (2n= 2x= 22). In: O'Brien SJ (ed)Genome maps. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, pp 259–261

Moe KT, Chung J, Cho Y et al (2011) Sequence information on simple sequence repeats and singlenucleotide polymorphisms through transcriptome analysis of mungbean. J Integr Plant Biol53:63–73

Moragues M, Comadran J, Waugh R et al (2010) Effects of ascertainment bias and marker numberon estimations of barley diversity from high-throughput SNP genotype data. TheorAppl Genet120:1525–1534

Morinaga T, Ikegami M, Miura K (1993) The nucleotide sequence and genome structure of mungbean yellow mosaic geminivirus. MicrobiolImmunol 37:471–476

Nair RM, Giri RR, Boddepalli VN, Prasad KVSV,Devulapalli R, Blümmel M (2019) Variation in grainyield, fodder quality and animal intake in two dualpurpose legume crops: mungbean and vegetablesoybean grown in semi-arid tropical India. LegumeRes. https://doi.org/10.18805/LR-4078

Nair R, Schafleitner R, Kenyon L et al (2012) Genetic improvement of mungbean. SABRAOJ Breed Genet 44:177–190

Oplinger E, Hardman L, Kaminski A et al (1990) Mungbean. In: Alternative field crop manual.University of Wisconsin Cooperative Extension Services, Madison

Pataczek L, Zahir Z, Ahmad M, Rani S, Nair R,Schafleitner R, Cadisch G, Hilger T (2018) Beanswith benefits—the role of mungbean (*Vignaradiata*)in a changing environment. Am J Plant Sci 9:1577–1600.

Pattnaik J, Kole C (2002) Detection of a protein markerfor screening of MYMV resistance mungbean genotype.Indian J Genet Plant Breed 62:77–78

Ran FA, Hsu PD, Wright J et al (2013) Genome engineering using the CRISPR-Cas9 system. NatProtoc 8:2281

Rao S, Patil P, Kaviraj C (2005) Callus induction and organogenesis from various explants in *Vignaradiata*(L.) Wilczek. Indian J Biotechnol 4:556–560

Raza MH, Sadozai GU, Baloch MS et al (2012) Effect of irrigation levels on growth and yield ofmungbean. Pak J Nutr 11(10):876

Sagare DB, Mohanty I (2015) *In vitro* regeneration system in green gram (*Vignaradiata*L.,Wilczek, cv. Sujata): a recalcitrant legume crop. Res J AgricSci 6:64–67

Sangiri C, Kaga A, Tomooka N et al (2008) Genetic diversity of the mungbean (*Vignaradiata*,Leguminosae) genepool on the basis of microsatellite analysis. Aust J Bot 55:837–847

Sangsiri C, Sorajjapinun W, Srinives P (2007) Inheritance and ultrastructure of variegated leafmutant in mungbean (*Vignaradiata*(L.) Wilczek). Thai J AgricSci 40:159–166

Santalla M, Power JB, Davey MR (1998) Genetic diversity in mungbean germplasm revealed by RAPD markers. Plant Breed 117:473–478

Schafleitner R, Huang SM, Chu SH, Yen JY, Lin CY, Yan MR, Long-fang OC et al (2016) Identification of single nucleotide polymorphism markers associated with resistance to bruchids (Callosobruchus spp.) in wild mungbean (*Vignaradiata* var. *sublobata*) and cultivated V. radiata through genotyping by sequencing and quantitative trait locus analysis. BMC Plant Biol 16:159

Schafleitner R, Nair RM, Rathore A et al (2015) The AVRDC–the world vegetable center mungbean(*Vignaradiata*) core and mini core collections. BMC Genomics 16:344

Selvi R, Muthiah AR, Manivannan N, Raveendran TS,Manickam A, Samiyappan R (2006) Tagging ofRAPD marker for MYMV resistance in mungbean(*Vignaradiata* (L.) Wilczek). Asian J Plant Sci 5(2):277–280

Shanmugasundaram S, Keatinge J, Hughes J d'A (2009) Counting on beans: mungbean improvementsin Asia. In: Spielman DJ, Pandya-Lorch R (eds) Millions fed proven successes in agriculturaldevelopment. IFPRI, Washington, DC, pp 103–108

Singh H, Joshi B, Chandel K et al (1975) Genetic diversity in some Asiatic *Phaseolus*species andits conservation. Indian J Genet Plant Breed 34A:52–57

Singh R, van Heusden AW, Yadav RC (2013) Acomparative genetic diversity analysis in mungbean(*Vignaradiata* L.) using inter-simple sequence repeat(ISSR) and amplified fragment length polymorphism(AFLP). Afr J Biotechnol 12:6574–6582

Sivakumar P, Gnanam R, Ramakrishnan K, Manickam A (2010) Somatic embryogenesis andregeneration of *Vignaradiata*. Biol Plant 54:245–251

Somta P, Raboy V, Srinives P (2012)Mapping of quantitative trait loci for phytic acid and

phosphorus contents in seed and seedling of mungbean(*Vignaradiata* (L.) Wilczek). Breed Sci 62(1):87–92

Somta P, Musch W, Kongsamai B et al (2008) New microsatellite markers isolated from mungbean(*Vignaradiata*(L.) Wilczek). MolEcolResour 8:1155–1157

Somta P, Seehalak W, Srinives P (2009) Development, characterization and cross-species amplification of mungbean (*Vignaradiata*) genic microsatellite markers. Conserv Genet 10(6):1939

Sonia N, Saini R, Singh RP, Jaiwal PK (2007) *Agrobacterium tumefaciens*mediated transfer of*Phaseolus vulgaris* alpha-amylase inhibitor-1 gene into mungbean *Vignaradiata*(L.) Wilczekusing bar as selectable marker. Plant Cell Rep 26:187–198

Srinives P, Kitsanachandee R, Chalee T, Sommanas W,Chanprame S (2010) Inheritance of resistance to irondeficiency and identification of AFLP markers associatedwith the resistance in mungbean (*Vignaradiata*(L.) Wilczek). Plant Soil 335:423–437

Stacey G, VandenBosch K (2005) "Translational" legume biology. Models to crops. Plant Physiol137:1173

Tah PR, Saxena S (2009) Induced synchrony in pod maturity in mungbean (*Vignaradiata*). IntJ AgricBiol 11:321–324

Talekar N (1988) Biology, damage and control of bruchid pests of mungbean. In:Shanmugasundaram S, McLean BT (eds) Mungbean: proceedings of the second internationalsymposium. AVRDC, Shanhua, pp 329–342

Tangphatsornruang S, Sangsrakru D, Chanprasert J,Uthaipaisanwong P, Yoocha T, Jomchai N, TragoonrungS (2009) The chloroplast genome sequence ofmungbean (*Vignaradiata*) determined by highthroughputpyrosequencing: structural organization and phylogenetic relationships. DNA Res 17:11–22

Tanksley SD, McCouch SR (1997) Seed banks and molecular maps: unlocking genetic potentialfrom the wild. Science 277:1063–1066

Tomooka N, Vaughan D, Kaga A (2005) Mungbean [*Vignaradiata*(L.) Wilczek]. Genet ResourChromEng Crop Improv Grain Legume 1:325–345

Van K, Kang YJ, Han KS, Lee YH, Gwag JG, Moon JK,Lee SH (2013) Genome-wide SNP discovery inmungbean by IlluminaHiSeq. TheorAppl Genet126(8):2017–2027

Varshney RK, Kudapa H, Pazhamala L et al (2015) Translational genomics in agriculture: someexamples in grain legumes. Crit Rev Plant Sci 34:169–194

Vijayan S, Kirti P (2012) Mungbean plants expressing *BjNPR1* exhibit enhanced resistance againstthe seedling rot pathogen, *Rhizoctoniasolani*. Transgenic Res 21:193–200

Vijayan S, Beena M, Kirti P (2006) Simple and effective regeneration of mungbean (*Vignaradiata*(L) Wilczek) using cotyledonary node explants. J Plant BiochemBiotechnol 15:131–134

Wang LX, Elbaidouri M, Abernathy B, Chen HL, Wang SH, Lee SH, Jackson SA, Cheng XZ(2015) Distribution and analysis of SSR in mung bean (*Vignaradiata*L.) genome based on anSSR-enriched library. Mol Breed 35(1)

Wani MR (2006) Estimates of genetic variability in mutated populations and the scope of selectionfor yield attributes in *Vignaradiata*(L.) Wilczek. Egypt J Biol 8:1–6

Yadav S, Gopala Krishna M, Maheswari M et al (2010) High frequency induction of multipleshoots and plant regeneration from cotyledonary node explant of mung bean (*Vignaradiata*LWilczek). J Plant BiochemBiotechnol 19:267–270

Yadav SK, Katikala S, Yellisetty V et al (2012) Optimization of *Agrobacterium* mediated genetictransformation of cotyledonary node explants of *Vignaradiata*. Springerplus 1:59

Young N, Kumar L, Menancio-Hautea D et al (1992) RFLP mapping of a major bruchid resistancegene in mungbean (*Vignaradiata*, L. Wilczek). TheorAppl Genet 84:839–844

Yu K, Park SJ, Poysa V (1999) Abundance and variation of microsatellite DNA sequences in beans(*Phaseolus*and *Vigna*). Genome 42:27–34

Zhou Z, Jiang Y, Wang Z et al (2015) Resequencing 302 wild and cultivated accessions identifiesgenes related to domestication and improvement in soybean. Nat Biotechnol 33:408–414